

10/591576

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SEQUENCE LISTING

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 TAKIO, Koji
 DOHMAE, Naoshi

<120> CHITIN OLIGOSACCHARIDE ELICITOR-BINDING PROTEINS

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<150> PCT/JP2005/003451

<151> 2005-03-02

<150> JP2004-59551

<151> 2004-03-03

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<170> PatentIn version 3.3

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Ser Pro Asn Ala Thr Thr Tyr Gly Asn Leu Val Ala Arg Phe Asn Thr	
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 210 215 220

Arg Ser Ser Ile Ser Asp Thr Ser Ala Asp His Asn Leu Met Leu Leu
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 245 250 255

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 290 295 300

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Thr Thr Ala Cys Gln Arg Gly Gly Ser Gly Arg Ser Gln Phe Ala Arg
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Lys Ile Pro Phe Arg Cys Arg Cys Asn Gly Asp Val Gly Gln Ser Asp	
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Leu	Pro	Val	Cys	Arg	Ser	Ser	Ile	Ser	Asp	Thr	Ser	Ala	Asp	His	Asn			
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tac	agt	ggt	tac	tcc	aac	agt	tca	tcg	ctc	atc	ata	caa	acc	agc	ctt			864
Tyr	Ser	Gly	Tyr	Ser	Asn	Ser	Ser	Ser	Leu	Ile	Ile	Gln	Thr	Ser	Leu			
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gtg	ttg	atc	att	atc	tgt	ttc	ctt	tga										987
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 Arg Leu Pro Ile Tyr Val Val Gln Pro Gln Asp Gly Leu Asp Ala Ile
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 Trp Ile Pro Leu Pro Cys Ser Cys Asp Lys Glu Glu Gly Ser Asn Val
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 Met His Leu Ala Tyr Ser Val Gly Lys Gly Glu Asn Thr Ser Ala Ile
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 195 200 205
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Lys Leu Gly Glu Thr Asn Gly Thr Gly Cys Gly Ser Thr Thr Cys Ala
 260 265 270

Tyr Ser Gly Tyr Ser Asn Ser Ser Ser Leu Ile Ile Gln Thr Ser Leu
 275 280 285

Ala Thr Asn Gln Thr Thr Ala Cys Gln Arg Gly Gly Ser Gly Arg Ser
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Met His Leu Ala Tyr Ser Val Gly Lys Gly Glu Asn Thr Ser Ala Ile	
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Ile Asp Asp Pro Thr Lys Leu Gln Met Gly Gln Ile Leu Asp Val Pro	
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Leu Pro Val Cys Arg Ser Ser Ile Ser Asp Thr Ser Ala Asp His Asn	
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100 105 110

Ala Asn Asn Ile Pro Asp Pro Asn Lys Ile Asn Val Ser Gln Thr Leu
115 120 125

Trp Ile Pro Leu Pro Cys Ser Cys Asp Lys Glu Glu Gly Ser Asn Val
130 135 140

Met His Leu Ala Tyr Ser Val Gly Lys Gly Glu Asn Thr Ser Ala Ile
145 150 155 160

Ala Ala Lys Tyr Gly Val Thr Glu Ser Thr Leu Leu Thr Arg Asn Lys
165 170 175

Ile Asp Asp Pro Thr Lys Leu Gln Met Gly Gln Ile Leu Asp Val Pro
180 185 190

Leu Pro Val Cys Arg Ser Ser Ile Ser Asp Thr Ser Ala Asp His Asn
195 200 205

Leu Met Leu Leu Pro Asp Gly Thr Tyr Gly Phe Thr Ala Gly Asn Cys
210 215 220

Ile Arg Cys Ser Cys Ser Ser Thr Thr Tyr Gln Leu Asn Cys Thr Ala
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245 250 255

Lys Leu Gly Glu Thr Asn Gly Thr Gly Cys Gly Ser Thr Thr Cys Ala
260 265 270

Tyr Ser Gly Tyr Ser Asn Ser Ser Ser Leu Ile Ile Gln Thr Ser Leu
275 280 285

Ala Thr Asn Gln Thr Thr Ala Cys Gln Arg Gly Gly Ser Gly Arg Ser
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Gln Phe

305

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Ile	Leu	Tyr	Thr	Ser	Pro	Val	Ala	Thr	Thr	Tyr	Gly	Asn	Xaa	Val	Ala
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Thr	Tyr	Leu	Ile	Ala	Ser	Lys
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 gctcatcata caaaccagcc ttgcaactaa tcagacaaca gcctgccaga gaggaggatc 180
 tgggagggtcg cagttcgcta ggtccatgtg gagcatgtct gttatctcct tccacatggt 240
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